



# results of BLAST

## BLASTP 2.2.8 [Jan-05-2004]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1081981467-19431-71379995229.BLASTQ3

### Query=

(160 letters)

**Database:** All non-redundant GenBank CDS

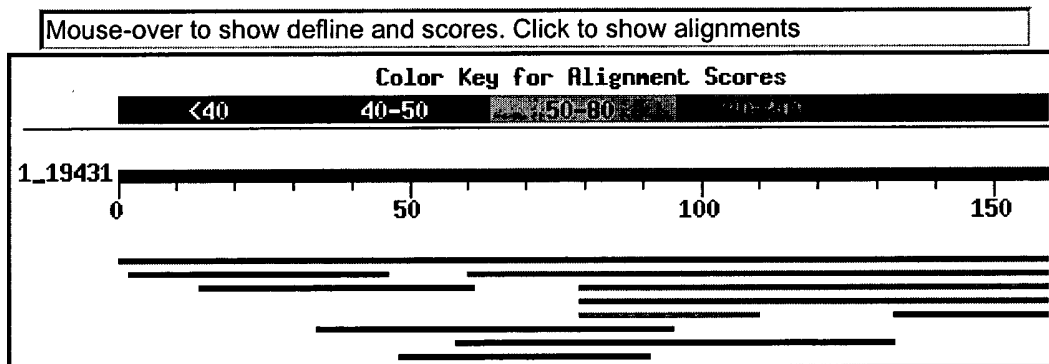
translations+PDB+SwissProt+PIR+PRF

2,763,327 sequences; 776,568,843 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 11 Blast Hits on the Query Sequence



Sequences producing significant alignments:		Score (bits)	E Value	
gi 19747281 ref NP_597674.1	G antigen, family D, 2 isoform...	291	2e-78	<a href="#">L</a>
gi 9966899 ref NP_065144.1	G antigen, family D, 2 isoform ...	175	4e-43	<a href="#">L</a>
gi 30585093 gb AAP36819.1	Homo sapiens G antigen, family D...	148	4e-35	
gi 13992499 emb CAC38107.1	9 kD cancer/testis associated p...	147	9e-35	<a href="#">L</a>
gi 19747279 ref NP_597673.1	G antigen, family D, 2 isoform...	62	3e-09	<a href="#">L</a>
gi 43770338 gb EAF39621.1	unknown [environmental sequence]	35	0.64	
gi 15227183 ref NP_179229.1	40S ribosomal protein S25 (RPS...	35	0.83	
gi 7191040 gb AAC15713.2	transcription factor Pax-A [Acrop...	33	1.6	

gi 19747283 ref NP_570133.1	G antigen, family D, 3; XAGE-2...	33	1.6	<b>L</b>
gi 23059365 ref ZP_00084339.1	COG1366: Anti-anti-sigma reg...	33	1.6	
gi 2463276 emb CAA74096.1	F420-reducing hydrogenase isoenz...	32	5.9	

### Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|19747281|ref|NP\_597674.1| **L** G antigen, family D, 2 isoform 1c; XAGE-1 protei  
gi|18157206|emb|CAC82986.1| **L** XAGE-1c protein [Homo sapiens]  
Length = 160

Score = 291 bits (746), Expect = 2e-78  
Identities = 160/160 (100%), Positives = 160/160 (100%)

Query: 1 MRCHAHGPSCLVTAITREEGGPRSGGAQAKLGCCWGYPSPRSTWNPDRRFWTPQTGPGE 60  
MRCHAHGPSCLVTAITREEGGPRSGGAQAKLGCCWGYPSPRSTWNPDRRFWTPQTGPGE  
Sbjct: 1 MRCHAHGPSCLVTAITREEGGPRSGGAQAKLGCCWGYPSPRSTWNPDRRFWTPQTGPGE 60

Query: 61 RHERHTQTQNHTASPRSPVMESPKKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICK 120  
RHERHTQTQNHTASPRSPVMESPKKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICK  
Sbjct: 61 RHERHTQTQNHTASPRSPVMESPKKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICK 120

Query: 121 SCISQTPGINLDLGSQVVKIIPKEEHCKMPEAGEEQPV 160  
SCISQTPGINLDLGSQVVKIIPKEEHCKMPEAGEEQPV  
Sbjct: 121 SCISQTPGINLDLGSQVVKIIPKEEHCKMPEAGEEQPV 160

☐ >gi|9966899|ref|NP\_065144.1| **L** G antigen, family D, 2 isoform 1a; XAGE-1 protei  
gi|17376379|sp|Q9HD64|GGD2 HUMAN **L** G antigen family D 2 protein (XAGE-1 protein)  
gi|9885325|gb|AAG01401.1| **L** XAGE-1 [Homo sapiens]  
Length = 146

Score = 175 bits (443), Expect = 4e-43  
Identities = 98/100 (98%), Positives = 98/100 (98%)

Query: 61 RHERHTQTQNHTASPRSPVMESPKKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICK 120  
RH HTQTQNHTASPRSPVMESPKKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICK  
Sbjct: 47 RHGGHTQTQNHTASPRSPVMESPKKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICK 106

Query: 121 SCISQTPGINLDLGSQVVKIIPKEEHCKMPEAGEEQPV 160  
SCISQTPGINLDLGSQVVKIIPKEEHCKMPEAGEEQPV  
Sbjct: 107 SCISQTPGINLDLGSQVVKIIPKEEHCKMPEAGEEQPV 146

←  
Alignment

☐ >gi|30585093|gb|AAP36819.1| Homo sapiens G antigen, family D, 2 [synthetic const  
Length = 82

Score = 148 bits (374), Expect = 4e-35  
Identities = 81/81 (100%), Positives = 81/81 (100%)

Query: 80 MESPKKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICKSCISQTPGINLDLGSQVVK 139

Sbjct: 1 MESPCKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICKSCISQTPGINLDLGSGVKV 60

Query: 140 KIIPKEEHCKMPEAGEEQPV 160

KIIPKEEHCKMPEAGEEQPV

Sbjct: 61 KIIPKEEHCKMPEAGEEQPV 81

☐ >gi|13992499|emb|CAC38107.1| ☒ 9 kD cancer/testis associated protein [Homo sapiens]  
gi|13992558|emb|CAC38108.1| ☒ cancer/testis-associated protein XAGE-1b [Homo sapiens]  
gi|16306935|gb|AAH09538.1| ☒ GAGED2 protein [Homo sapiens]  
gi|30583037|gb|AAP35763.1| G antigen, family D, 2 [Homo sapiens]  
Length = 81

Score = 147 bits (370), Expect = 9e-35  
Identities = 81/81 (100%), Positives = 81/81 (100%)

Query: 80 MESPCKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICKSCISQTPGINLDLGSGVKV 139

MESPCKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICKSCISQTPGINLDLGSGVKV

Sbjct: 1 MESPCKKNQQLKVGILHLGSRQKKIRIQLRSQCATWKVICKSCISQTPGINLDLGSGVKV 60

Query: 140 KIIPKEEHCKMPEAGEEQPV 160

KIIPKEEHCKMPEAGEEQPV

Sbjct: 61 KIIPKEEHCKMPEAGEEQPV 81

☐ >gi|19747279|ref|NP\_597673.1| ☒ G antigen, family D, 2 isoform 1d; XAGE-1 protein [Homo sapiens]  
gi|18157208|emb|CAC82987.1| ☒ XAGE-1d protein [Homo sapiens]  
Length = 69

Score = 62.4 bits (150), Expect = 3e-09  
Identities = 32/32 (100%), Positives = 32/32 (100%)

Query: 80 MESPCKKNQQLKVGILHLGSRQKKIRIQLRSQ 111

MESPCKKNQQLKVGILHLGSRQKKIRIQLRSQ

Sbjct: 1 MESPCKKNQQLKVGILHLGSRQKKIRIQLRSQ 32

☐ >gi|43770338|gb|EAF39621.1| unknown [environmental sequence]  
Length = 315

Score = 35.0 bits (79), Expect = 0.64  
Identities = 20/67 (29%), Positives = 32/67 (47%), Gaps = 8/67 (11%)

Query: 35 WGYSPRSTWNPDRRFWTPQTGPGEGR-----HERHTQTQNHTASPRSPVMESPCKKNQQ 89

W Y S ++ W ++R+W +T E R HE T+T R+ V+ K++ +

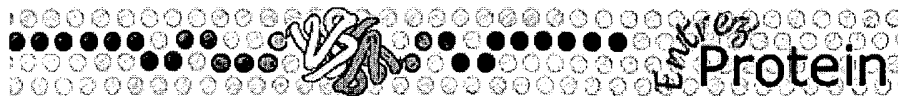
Sbjct: 15 WSYVSNKNNWVENQRYWIEKTKHLEDRLSDRLHEELTKT---FIDKRASVLARGLKQDME 71

Query: 90 LKVGILH 96

K ILH

Sbjct: 72 FKTEILH 78

☐ >gi|15227183|ref|NP\_179229.1| 40S ribosomal protein S25 (RPS25A) [Arabidopsis thaliana]



Entrez

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Book

Search

Protein

for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display

GenPept

Show:

20

Send to

File

Get Subsequence

Feature

☐ 1: NP\_065144. G antigen, family...[gi:9966899]

BLink, Links

LOCUS NP\_065144 146 aa linear PRI 21-DEC-2003  
 DEFINITION G antigen, family D, 2 isoform 1a; XAGE-1 protein [Homo sapiens].  
 ACCESSION NP\_065144  
 VERSION NP\_065144.1 GI:9966899  
 DBSOURCE REFSEQ: accession NM\_020411.1  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 146)  
 AUTHORS Egland,K.A., Kumar,V., Duray,P. and Pastan,I.  
 TITLE Characterization of overlapping XAGE-1 transcripts encoding a cancer testis antigen expressed in lung, breast, and other types of cancers  
 JOURNAL Mol. Cancer Ther. 1 (7), 441-450 (2002)  
 PUBMED 12479262  
 REMARK GeneRIF: transcription of the XAGE-1 gene is initiated from two distinct start sites, resulting in two overlapping transcripts, XAGE-1a and XAGE-1b; XAGE-1 is expressed in a diverse range of cancers

REFERENCE 2 (residues 1 to 146)  
 AUTHORS Zendman,A.J., Van Kraats,A.A., Weidle,U.H., Ruiter,D.J. and Van Muijen,G.N.  
 TITLE The XAGE family of cancer/testis-associated genes: alignment and expression profile in normal tissues, melanoma lesions and Ewing's sarcoma  
 JOURNAL Int. J. Cancer 99 (3), 361-369 (2002)  
 PUBMED 11992404  
 REMARK GeneRIF: The XAGE family of cancer/testis-associated genes: alignment and expression profile in normal tissues, melanoma lesions and Ewing's sarcoma

REFERENCE 3 (residues 1 to 146)  
 AUTHORS Zendman,A.J., van Kraats,A.A., den Hollander,A.I., Weidle,U.H., Ruiter,D.J. and van Muijen,G.N.  
 TITLE Characterization of XAGE-1b, a short major transcript of cancer/testis-associated gene XAGE-1, induced in melanoma metastasis  
 JOURNAL Int. J. Cancer 97 (2), 195-204 (2002)  
 PUBMED 11774264

REFERENCE 4 (residues 1 to 146)  
 AUTHORS Liu,X.F., Helman,L.J., Yeung,C., Bera,T.K., Lee,B. and Pastan,I.  
 TITLE XAGE-1, a new gene that is frequently expressed in Ewing's sarcoma  
 JOURNAL Cancer Res. 60 (17), 4752-4755 (2000)  
 PUBMED 10987281

REFERENCE 5 (residues 1 to 146)  
 AUTHORS Brinkmann,U., Vasmatazis,G., Lee,B. and Pastan,I.  
 TITLE Novel genes in the PAGE and GAGE family of tumor antigens found by homology walking in the dbEST database

JOURNAL Cancer Res. 59 (7), 1445-1448 (1999)  
PUBMED [10197611](#)  
COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [AF251237.1](#).

Summary: This gene is a member of the XAGE subfamily, which belongs to the GAGE family. The GAGE genes are expressed in a variety of tumors and in some fetal and reproductive tissues. This gene is strongly expressed in Ewing's sarcoma, alveolar rhabdomyosarcoma and normal testis. The protein encoded by this gene contains a nuclear localization signal and shares a sequence similarity with other GAGE/PAGE proteins. Because of the expression pattern and the sequence similarity, this protein also belongs to a family of CT (cancer-testis) antigens. Alternative splicing of this gene generates 3 transcript variants, and one of which includes 2 transcripts generated from alternate transcription initiation sites.

Transcript Variant: This variant (1) includes 2 transcripts with different sizes. The longer transcript encodes isoform (1a). The shorter transcript is the major product of the gene. Its ORF is in-frame with the longer transcript but encodes an N-terminal truncated isoform (1b), as compared to isoform (1a).

FEATURES                      Location/Qualifiers  
    source                      1..146  
                                /organism="Homo sapiens"  
                                /db\_xref="taxon:9606"  
                                /chromosome="X"  
                                /map="Xp11.22-p11.21"  
    Protein                      1..146  
                                /product="G antigen, family D, 2 isoform 1a"  
                                /note="XAGE-1 protein"  
    Region                      66..146  
                                /region\_name="isoform 1b encoded by the short transcript"  
                                /note="XAGE-1b"  
    Region                      70..89  
                                /region\_name="nuclear localization signal"  
    CDS                          1..146  
                                /gene="GAGED2"  
                                /coded\_by="NM\_020411.1:86..526"  
                                /note="XAGE-1 protein  
                                isoform 1a is encoded by transcript variant 1"  
                                /db\_xref="GeneID:9503"  
                                /db\_xref="LocusID:9503"  
                                /db\_xref="MIM:300289"

## ORIGIN

1 mllwcppqca cslgvfpsap spvwgtrrsc epatrpevw ilspllrhgg htqtqnhtas  
61 prspvmespk kknqqlkvgi lhlgsrqkki riqlrsqcat wkvickscis qtpginldlg  
121 sgkvkiiipk eehckmpeag eeppqv

//